In the Claims:

Please cancel claims 40-80. Please add the following new claims.

Claims 1-39 (PREVIOUSLY CANCELLED).

Claims 40-80 (CURRENTLY CANCELLED).

Claim 81 (NEW). A ligase-mediated method of *in vitro* recombination, comprising:

providing oligonucleotide cleavage fragments derived from each of at least two different polynucleotides of a polynucleotide library;

hybridizing the cleavage fragments to an assembly template;

ligating together the hybridized fragments that have adjacent ends with a ligase;

denaturing the ligated fragments from the assembly template; and

repeating at least the hybridizing, ligating and denaturing steps multiple times to form a recombinant polynucleotide comprised of the ligated fragments.

Claim 82 (NEW). The method of claim 81, wherein the method is performed in the absence of polymerase.

Claim 83 (NEW). The method of claim 81, wherein any polymerase used in the method is used only to amplify the number of copies of: the different polynucleotides, the cleavage fragments, the formed recombinant polynucleotide, the assembly template or a combination of the foregoing.

Claim 84 (NEW). The method of claim 81, wherein any polymerase used in the method is used only to increase the number of copies of the cleavage fragments, the formed recombinant polynucleotide, or both.

Claim 85 (NEW). The method of claim 81, wherein the recombinant polynucleotide formed by the method is new and possesses advantageous properties compared to a reference sequence.

Claim 86 (NEW). The method of claim 81, wherein the hybridizing and ligating steps are carried out simultaneously.

Claim 87 (NEW). The method of claim 81, wherein the cleavage fragments are obtained by cleavage of said different polynucleotides.

Claim 88 (NEW). The method of claim 87, wherein the cleavage is random cleavage.

Claim 89 (NEW). The method of claim 88, wherein said random cleavage comprises treating said different polynucleotides with DNAse I.

Claim 90 (NEW). The method of claim 81, wherein the step of providing the cleavage fragments comprises hydrolyzing said different polynucleotides with restriction enzymes.

Claim 91 (NEW). The method of claim 90, wherein the hydrolyzing is performed with several different restriction enzymes or with restriction enzymes that have a plurality of different cutting sites on the polynucleotides from the library.

Claim 92 (NEW). The method of claim 91, wherein the hydrolyzing comprises separately hydrolyzing different polynucleotides from at least two distinct polynucleotide libraries by subjecting the distinct libraries to different restriction enzymes.

Claim 93 (NEW). The method of claim 81, further comprising adding degrading enzymes that recognize and cut non-hybridized ends of the hybridized fragments in a specific manner when the non-hybridized ends overlap other hybridized fragments on the same assembly template.

Claim 94 (NEW). The method of claim 93, wherein the degrading enzyme is a flap endonuclease.

Claim 95 (NEW). The method of claim 94, wherein said ligase is thermostable and active at the temperature necessary for the hybridization step.

Claim 96 (NEW). The method of claim 95, wherein the degrading enzyme is thermostable and active at the temperature necessary for the hybridization step.

Claim 97 (NEW). The method of claim 81, further comprising adding additional assembly templates before formation of the recombinant polynucleotide.

Claim 98 (NEW). The method of claim 81, wherein one or more of the cleavage fragments serve as the assembly template.

Claim 99 (NEW). The method of claim 81, wherein said different polynucleotides or the cleavage fragments derived therefrom are double-stranded and must be denatured before the hybridizing step.

Claim 100 (NEW). The method of claim 81, further comprising selecting the formed recombinant polynucleotide that possesses advantageous properties compared to a reference sequence.

Claim 101 (NEW). The method of claim 81, further comprising cloning the formed recombinant polynucleotide.

Claim 102 (NEW). The method of claim 81, wherein the assembly template comprises oligonucleotides that are complementary to the 3' ends of a plurality of the cleavage fragments and to the 5' ends of a plurality of other of the cleavage fragments.

Claim 103 (NEW). The method of claim 81, wherein substantial portions of said different polynucleotides are homologous to each other.

Claim 104 (NEW). The method of claim 81, wherein a plurality of the cleavage fragments are complementary to portions of the assembly template that are adjacent to each other.

Claim 105 (NEW). The method of claim 81, wherein the polynucleotide library comprises artificial polynucleotides.

Claim 106 (NEW). A ligation-mediated method of *in vitro* recombination, comprising:

hybridizing, to an assembly template, fragments of polynucleotides derived from a polynucleotide library comprised of at least two different polynucleotides;

ligating together those hybridized fragments that have adjacent ends with a ligase;

denaturing the ligated fragments from the assembly template, and

repeating the hybridizing, ligating and denaturing steps multiple times, thereby forming a recombinant polynucleotide comprised of the ligated fragments,

wherein the method is performed in the absence of a polymerase.

Claim 107 (NEW). A ligation-mediated method of *in vitro* recombination, comprising:

providing cleavage fragments of polynucleotides from a polynucleotide library comprised of at least two different polynucleotides;

hybridizing the cleavage fragments to an assembly template;

ligating together those hybridized fragments that have adjacent ends with a ligase;

denaturing the ligated fragments from the assembly template, and

repeating the hybridizing, ligating and denaturing steps multiple times, thereby forming a new recombinant polynucleotide comprised of the ligated fragments,

wherein any polymerase used in the method is used only to amplify the number of copies of: the different polynucleotides, the cleavage fragments, the formed recombinant polynucleotide, the assembly template or a combination of the foregoing.